RECEIVED P#9

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TECH CENTER 1600/2900

RAW SEQUENCE LISTING   DATE: 05/21/2001
PATENT APPLICATION: US/09/698,213A   TIME: 10:43:56

ENTERED

Input Set : A:\SeqList.txt
Output Set: N:\CRF3\05212001\I698213A.raw

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 2 <110> APPLICANT: McIninch, James
 4 <120> TITLE OF INVENTION: COMPUTATIONAL NUCLEIC ACID CODING AND FEATURE ANALYSIS
 6 <130> FILE REFERENCE: 04983.0220.00US00
 8 <140> CURRENT APPLICATION NUMBER: 09/698,213A
10 <141> CURRENT FILING DATE: 2000-10-30
12 <160> NUMBER OF SEQ ID NOS: 13
14 <170> SOFTWARE: PatentIn version 3.0
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 2165
18 <212> TYPE: DNA
19 <213> ORGANISM: Arabidopsis thaliana
21 <220> FEATURE:
22 <221> NAME/KEY: unsure
23 <222> LOCATION: (1)...(2165)
24 <223> OTHER INFORMATION: Unsure at all n locations
26 <220> FEATURE:
27 <223> OTHER INFORMATION: Ecotype Landsberg, genomic DNA
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34 aaaaggatgc ttatgttgga gacgaggctc aatcaaaacg tggtatcttg actctgaagt     180
36 acccaattga gcatggaatt gttaataatt gggatgacat ggagaagatt tggcatcaca     240
38 ctttctacaa tgagcttcgt gttgcccctg aagaacatcc ggttctcttg accgaagctc     300
40 ctctcaatcc gaaagctaac cgtgagaaga tgactcagat catgtttgag acattcaata     360
42 ctcctgctat gtatgttgcc attcaagctg ttctctcact ctatgccagt ggccgtacta     420
44 ctggtcagta cattactaca ttcttttat accgtttggt tgaaataaaa ttcggtttgg      480
46 ttcgattcga gtttgctctc attatttta ttttgttggt taggtattgt tttggactcc     540
48 ggagatggtg tgagccacac ggtaccaatc tacgagggtt atgcacttcc acacgcaatc     600
50 ctgcgtcttg atcttgcagg tcgtgaccta accgaccacc ttatgaaaat cctgacagag     660
52 cgtggttact ctttcaccac aactgctgag cgtgagattg ttagagacat gaaggagaag     720
54 ctctcttaca ttgccttgga ctttgaacaa gagctcgaga cttccaaaac aagctcatcc     780
56 gttgagaaga gcttcgagct gccagacggt caagtgatca ccatcggggc agagcgtttc     840
58 cgatgccctg aagttctgtt tcagccatcg atgatcggaa tggaaaatcc gggaattcat     900
60 gaaactactt acaactcaat catgaaatgt gatgtggata tcaggaagga tctttatgga     960
62 aacattgtgc ttagtggtgg caccacaatg ttcgatggga ttggtgatag gatgagtaaa    1020
64 gagatcacag cgttggctcc aagcagtatg aacatcaaag tggtggctcc accggaaagg    1080
66 aagtacagtg tctggatcgg tggctctatc ttggcttccc tcagtacttt ccagcaggta    1140
68 aattacttac tatacttaat acataaagtc tattagtgat ttgatgtata aagtgttaca    1200
70 aaaatgtgtt ccaaatttgc agatgtggat tgcgaaagcg gagtatgatg aatctggacc    1260
72 gtcaatcgtc cacaggaagt gcttctgatc aaaagtcacc aagtaaaaca agagcggtaa    1320
74 aaattttgat atcagttttt caccctgaag ccagttgcta taattactca caacttctct    1380
76 atttgtgttc ttttattctt gtccctcgtt gttcatttta atctctttt tgcaacaaag     1440
78 caacttaaaa aaacagagca gtcattaaca gaatgttatt attatatata tgtatacata    1500
80 ttagtataca cccattattt cattaaaaca tttatcatat aaggatagga ttctatacat    1560
82 cgatatattt attttgttga cactattcag cacatgctta tgtcttatct tgttagtata    1620
84 tgtaaccaaa gacaaataat agatgctaca aattgttttc tttgaagcaa aaatttcaat    1680
86 cttaaaattg ttttttttcca ggttacacaa aaaaaacttg tagtttgtaa attttctata    1740
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5/21/01

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 88 caattttggg gatctcaaca agaacatgaa cttcaacttc tagtcatatg acgacctgag    1800
 90 tctgcgcggc tgtgaatctc tttgctgcag taaatgttta caagtggtgt gtaaattggt    1860
 92 actgattcaa aagctttaag aaatctacac atttcgtgaa attatttagc agacttgata    1920
 94 ttaaaaatct aggataaaat gactatccaa agacaaatag gactgtttca catgttcccc    1980
 96 tgattcttgt agctcataac tcatcagcag ttaacttttc tacctcatac acgctcgcaa    2040
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119 <211> LENGTH: 7
120 <212> TYPE: PRT
121 <213> ORGANISM: Unknown
123 <220> FEATURE:
124 <223> OTHER INFORMATION: Describes a predicted protein sequence
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132 <211> LENGTH: 21
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134 <213> ORGANISM: Unknown
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148 <211> LENGTH: 35
149 <212> TYPE: PRT
150 <213> ORGANISM: Unknown
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153 <223> OTHER INFORMATION: Describes a predicted protein sequence
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167 <211> LENGTH: 56
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169 <213> ORGANISM: Unknown
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178 Gln Ile Met Phe Glu Thr Phe Asn Thr Pro Ala Met Tyr Val Ala Ile
179             20                  25                  30
181 Gln Ala Val Leu Ser Leu Tyr Ala Ser Gly Arg Thr Thr Gly Gln Tyr
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189 <211> LENGTH: 191
190 <212> TYPE: PRT
191 <213> ORGANISM: Unknown
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Describes a predicted protein sequence
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200 Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr
201             20                  25                  30
203 Asp His Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr
204         35                  40                  45
206 Thr Ala Glu Arg Glu Ile Val Arg Asp Met Lys Glu Lys Leu Ser Tyr
207     50                  55                  60
209 Ile Ala Leu Asp Phe Glu Gln Glu Leu Glu Thr Ser Lys Thr Ser Ser
210 65                  70                  75                  80
212 Ser Val Glu Lys Ser Phe Glu Leu Pro Asp Gly Gln Val Ile Thr Ile
213                 85                  90                  95
215 Gly Ala Glu Arg Phe Arg Cys Pro Glu Val Leu Phe Gln Pro Ser Met
216             100                 105                 110
218 Ile Gly Met Glu Asn Pro Gly Ile His Glu Thr Thr Tyr Asn Ser Ile
219         115                 120                 125
221 Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val
222     130                 135                 140
224 Leu Ser Gly Gly Thr Thr Met Phe Asp Gly Ile Gly Asp Arg Met Ser
225 145                 150                 155                 160
227 Lys Glu Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val
228                 165                 170                 175
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236 <212> TYPE: PRT
237 <213> ORGANISM: Unknown
239 <220> FEATURE:
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248 <211> LENGTH: 26
249 <212> TYPE: PRT
250 <213> ORGANISM: Unknown
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Describes a predicted protein sequence
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260              20                  25
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264 <211> LENGTH: 56
265 <212> TYPE: PRT
266 <213> ORGANISM: Unknown
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Describes a predicted protein sequence
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277              20                  25                  30
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287 <211> LENGTH: 194
288 <212> TYPE: PRT
289 <213> ORGANISM: Unknown
291 <220> FEATURE:
292 <223> OTHER INFORMATION: Describes a predicted protein sequence
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298 Leu Pro His Ala Ile Leu Arg Leu Asp Leu Ala Gly Arg Asp Leu Thr
299              20                  25                  30
301 Asp His Leu Met Lys Ile Leu Thr Glu Arg Gly Tyr Ser Phe Thr Thr
302         35                  40                  45
304 Thr Ala Glu Arg Glu Ile Val Arg Asp Met Lys Glu Lys Leu Ser Tyr
305      50                  55                  60
307 Ile Ala Leu Asp Phe Glu Gln Glu Leu Glu Thr Ser Lys Thr Ser Ser
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308 65                      70              75              80
310 Ser Val Glu Lys Ser Phe Glu Leu Pro Asp Gly Gln Val Ile Thr Ile
311           85              90              95
313 Gly Ala Glu Arg Phe Arg Cys Pro Glu Val Leu Phe Gln Pro Ser Met
314           100             105             110
316 Ile Gly Met Glu Asn Pro Gly Ile His Glu Thr Thr Tyr Asn Ser Ile
317           115             120             125
319 Met Lys Cys Asp Val Asp Ile Arg Lys Asp Leu Tyr Gly Asn Ile Val
320       130             135             140
322 Leu Ser Gly Gly Thr Thr Met Phe Asp Gly Ile Gly Asp Arg Met Ser
323 145             150             155             160
325 Lys Glu Ile Thr Ala Leu Ala Pro Ser Ser Met Lys Ile Lys Val Val
326           165             170             175
328 Ala Pro Pro Glu Arg Lys Tyr Ser Val Trp Ile Gly Gly Ser Ile Leu
329           180             185             190
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334 <210> SEQ ID NO: 12
335 <211> LENGTH: 9
336 <212> TYPE: PRT
337 <213> ORGANISM: Unknown
339 <220> FEATURE:
340 <223> OTHER INFORMATION: Describes a predicted protein sequence
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347 <210> SEQ ID NO: 13
348 <211> LENGTH: 296
349 <212> TYPE: PRT
350 <213> ORGANISM: Arabidopsis thaliana
352 <220> FEATURE:
353 <223> OTHER INFORMATION: Ecotype columbia, describes actin
355 <400> SEQUENCE: 13
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361           20              25              30
363 Ala Asn Arg Glu Lys Met Thr Gln Ile Met Phe Glu Thr Phe Asn Thr
364           35              40              45
366 Pro Ala Met Tyr Val Ala Ile Gln Ala Val Leu Ser Leu Ala Ser Gly
367       50              55              60
369 Arg Thr Thr Gly Gly Ile Val Leu Asp Ser Gly Asp Gly Val Ser His
370 65              70              75              80
372 Thr Val Pro Ile Tyr Glu Gly Tyr Ala Leu Pro His Ala Ile Leu Arg
373           85              90              95
375 Leu Asp Leu Ala Gly Arg Asp Leu Thr Asp His Leu Met Lys Ile Leu
376           100             105             110
378 Thr Glu Arg Gly Tyr Ser Phe Thr Thr Thr Ala Glu Arg Glu Ile Val
379           115             120             125
381 Arg Asp Met Lys Glu Lys Leu Ser Tyr Ile Ala Leu Asp Phe Glu Gln
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VERIFICATION SUMMARY
PATENT APPLICATION: US/09/698,213A

DATE: 05/21/2001
TIME: 10:43:57

Input Set : A:\SeqList.txt
Output Set: N:\CRF3\05212001\I698213A.raw

L:98 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1